

Category	Term	Count	%	PValue	Genes
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	10	7.04225352	1.55E-08	COL4A4, COL4A2, COL4A1, LAMA5, NPNT, ITGB6, DAG1, LAMC2, LAMC1, AGRN
KEGG_PATHWAY	mmu04510:Focal adhesion	13	9.15492958	3.70E-08	EGFR, COL4A4, ACTB, CAV2, CAV1, COL4A2, COL4A1, LAMA5, VEGFA, ITGB6, RHOA, LAMC2, LAMC1
KEGG_PATHWAY	mmu04530:Tight junction	11	7.74647887	9.19E-08	ACTB, PARD6B, MAGI3, TJP1, CLDN18, MAGI1, SPNB2, MPP5, RHOA, MYH9, CTNNA1
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	9	6.33802817	3.23E-04	ACTB, EGFR, GSN, ITGB6, RHOA, TMSB4X, MSN, MYH9, F2R
KEGG_PATHWAY	mmu04520:Adherens junction	6	4.22535211	3.55E-04	ACTB, EGFR, TJP1, RHOA, LMO7, CTNNA1
KEGG_PATHWAY	mmu05222:Small cell lung cancer	6	4.22535211	5.96E-04	COL4A4, COL4A2, COL4A1, LAMA5, LAMC2, LAMC1
KEGG_PATHWAY	mmu05200:Pathways in cancer	10	7.04225352	0.00103309	EGFR, COL4A4, COL4A2, COL4A1, LAMA5, VEGFA, RHOA, LAMC2, LAMC1, CTNNA1
KEGG_PATHWAY	mmu05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	5	3.52112676	0.00313971	ACTB, ITGB6, DAG1, GJA1, CTNNA1
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	5	3.52112676	0.01579098	ACTB, CLDN18, RHOA, MSN, CTNNA1
KEGG_PATHWAY	mmu04144:Endocytosis	6	4.22535211	0.02379123	EGFR, PARD6B, WWP1, RAB11FIP1, EHD2, F2R
KEGG_PATHWAY	mmu05416:Viral myocarditis	4	2.81690141	0.04111116	ACTB, CAV1, DAG1, MYH9

List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
48	83	5738	14.40261044	9.80E-07	9.80E-07	1.57E-05
48	198	5738	7.848695286	2.33E-06	1.16E-06	3.74E-05
48	135	5738	9.740432099	5.79E-06	1.93E-06	9.30E-05
48	217	5738	4.957949309	0.0201613	0.00507889	0.32681423
48	76	5738	9.4375	0.02210521	0.00446066	0.35862255
48	85	5738	8.438235294	0.03687277	0.00624206	0.6020129
48	323	5738	3.700980392	0.0630432	0.00925945	1.04113958
48	75	5738	7.969444444	0.17972294	0.02446002	3.13397291
48	119	5738	5.022759104	0.63313825	0.10543607	14.88511
48	202	5738	3.550742574	0.78062329	0.14075097	21.6364342
48	94	5738	5.086879433	0.92897675	0.2137116	34.6277105

Annotation Cluster 1	Enrichment Score: 7.227894603165832			
Category	Term	Count	%	PValue
GOTERM_CC_FA T	GO:0005604~basement membrane	13	9.15492958	9.77E-13
GOTERM_CC_FA T	GO:0044420~extracellular matrix part	13	9.15492958	1.69E-11
GOTERM_CC_FA T	GO:0031012~extracellular matrix	16	11.2676056	5.42E-08
GOTERM_CC_FA T	GO:0005578~proteinaceous extracellular matrix	15	10.5633803	2.24E-07
GOTERM_CC_FA T	GO:0044421~extracellular region part	18	12.6760563	2.91E-04
GOTERM_CC_FA T	GO:0005576~extracellular region	28	19.7183099	7.36E-04

Annotation Cluster 2	Enrichment Score: 4.295415322088468			
Category	Term	Count	%	PValue
GOTERM_CC_FA T	GO:0005587~collagen type IV	4	2.81690141	1.20E-05
GOTERM_CC_FA T	GO:0030935~sheet-forming collagen	4	2.81690141	1.20E-05
GOTERM_MF_FA T	GO:0005201~extracellular matrix structural constituent	5	3.52112676	8.61E-05
GOTERM_CC_FA T	GO:0005581~collagen	4	2.81690141	5.34E-04

Annotation Cluster 3	Enrichment Score: 4.125314720217833			
Category	Term	Count	%	PValue
GOTERM_BP_FA T	GO:0006928~cell motion	13	9.15492958	1.27E-05
GOTERM_BP_FA T	GO:0016477~cell migration	10	7.04225352	5.78E-05
GOTERM_BP_FA T	GO:0051674~localization of cell	10	7.04225352	2.08E-04
GOTERM_BP_FA T	GO:0048870~cell motility	10	7.04225352	2.08E-04

Annotation Cluster 4	Enrichment Score: 3.8438926623361422			
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Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0030029~actin filament-based process	10	7.04225352	4.90E-06
GOTERM_BP_FA_T	GO:0030036~actin cytoskeleton organization	9	6.33802817	2.48E-05
GOTERM_MF_FA_T	GO:0008092~cytoskeletal protein binding	13	9.15492958	1.02E-04
GOTERM_MF_FA_T	GO:0003779~actin binding	9	6.33802817	0.00200343
GOTERM_BP_FA_T	GO:0007010~cytoskeleton organization	9	6.33802817	0.00243832

Annotation Cluster 5	Enrichment Score: 3.7884871971334775			
Category	Term	Count	%	PValue
GOTERM_CC_FA_T	GO:0005911~cell-cell junction	11	7.74647887	2.19E-06
GOTERM_CC_FA_T	GO:0043296~apical junction complex	7	4.92957746	2.24E-04
GOTERM_CC_FA_T	GO:0016327~apicolateral plasma membrane	7	4.92957746	2.49E-04
GOTERM_CC_FA_T	GO:0005923~tight junction	6	4.22535211	4.76E-04
GOTERM_CC_FA_T	GO:0070160~occluding junction	6	4.22535211	4.76E-04
GOTERM_CC_FA_T	GO:0030054~cell junction	13	9.15492958	6.71E-04

Annotation Cluster 6	Enrichment Score: 3.0194335162550296			
Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0060541~respiratory system development	10	7.04225352	2.61E-07
GOTERM_BP_FA_T	GO:0030324~lung development	9	6.33802817	1.31E-06
GOTERM_BP_FA_T	GO:0030323~respiratory tube development	9	6.33802817	1.51E-06
GOTERM_BP_FA_T	GO:0035295~tube development	11	7.74647887	2.02E-05
GOTERM_BP_FA_T	GO:0007435~salivary gland morphogenesis	4	2.81690141	9.38E-04
GOTERM_BP_FA_T	GO:0007431~salivary gland development	4	2.81690141	0.00141234
GOTERM_BP_FA_T	GO:0035239~tube morphogenesis	7	4.92957746	0.00147337

GOTERM_BP_FA_T	GO:0001763~morphogenesis of a branching structure	6	4.22535211	0.00208749
GOTERM_BP_FA_T	GO:0048732~gland development	7	4.92957746	0.00300171
GOTERM_BP_FA_T	GO:0022612~gland morphogenesis	5	3.52112676	0.0031587
GOTERM_BP_FA_T	GO:0035272~exocrine system development	4	2.81690141	0.00317946
GOTERM_BP_FA_T	GO:0060429~epithelium development	8	5.63380282	0.0034335
GOTERM_BP_FA_T	GO:0048754~branching morphogenesis of a tube	5	3.52112676	0.00455038
GOTERM_BP_FA_T	GO:0030155~regulation of cell adhesion	5	3.52112676	0.00472674
GOTERM_BP_FA_T	GO:0060445~branching involved in salivary gland morphogenesis	3	2.11267606	0.00730689
GOTERM_BP_FA_T	GO:0002009~morphogenesis of an epithelium	5	3.52112676	0.03643064
GOTERM_BP_FA_T	GO:0048729~tissue morphogenesis	5	3.52112676	0.0932387
GOTERM_BP_FA_T	GO:0060562~epithelial tube morphogenesis	3	2.11267606	0.19083838

Annotation Cluster 7	Enrichment Score: 2.9909142786382716			
Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0007519~skeletal muscle tissue development	7	4.92957746	1.28E-05
GOTERM_BP_FA_T	GO:0060538~skeletal muscle organ development	7	4.92957746	1.50E-05
GOTERM_BP_FA_T	GO:0007517~muscle organ development	9	6.33802817	3.94E-05
GOTERM_BP_FA_T	GO:0014706~striated muscle tissue development	7	4.92957746	3.09E-04
GOTERM_BP_FA_T	GO:0060537~muscle tissue development	7	4.92957746	4.46E-04
GOTERM_BP_FA_T	GO:0048741~skeletal muscle fiber development	4	2.81690141	0.00155034
GOTERM_BP_FA_T	GO:0042692~muscle cell differentiation	6	4.22535211	0.00156021
GOTERM_BP_FA_T	GO:0048747~muscle fiber development	4	2.81690141	0.0025557
GOTERM_BP_FA_T	GO:0051146~striated muscle cell differentiation	5	3.52112676	0.0038893
GOTERM_BP_FA_T	GO:0055002~striated muscle cell development	4	2.81690141	0.00691555

GOTERM_BP_FA_T	GO:0055001~muscle cell development	4	2.81690141	0.00967756
GOTERM_CC_FA_T	GO:0045202~synapse	3	2.11267606	0.76197082

Annotation Cluster 8	Enrichment Score: 2.9541672855845693			
Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0032989~cellular component morphogenesis	12	8.45070423	4.40E-05
GOTERM_BP_FA_T	GO:0000902~cell morphogenesis	10	7.04225352	3.87E-04
GOTERM_BP_FA_T	GO:0030030~cell projection organization	6	4.22535211	0.08074215

Annotation Cluster 9	Enrichment Score: 2.822320234388309			
Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0044087~regulation of cellular component biogenesis	9	6.33802817	2.39E-07
GOTERM_BP_FA_T	GO:0032271~regulation of protein polymerization	6	4.22535211	5.48E-05
GOTERM_BP_FA_T	GO:0051493~regulation of cytoskeleton organization	7	4.92957746	7.87E-05
GOTERM_BP_FA_T	GO:0043254~regulation of protein complex assembly	6	4.22535211	1.03E-04
GOTERM_BP_FA_T	GO:0051129~negative regulation of cellular component organization	6	4.22535211	5.54E-04
GOTERM_BP_FA_T	GO:0030837~negative regulation of actin filament polymerization	4	2.81690141	7.46E-04
GOTERM_BP_FA_T	GO:0033043~regulation of organelle organization	7	4.92957746	8.58E-04
GOTERM_BP_FA_T	GO:0032956~regulation of actin cytoskeleton organization	5	3.52112676	9.11E-04
GOTERM_BP_FA_T	GO:0032272~negative regulation of protein polymerization	4	2.81690141	9.38E-04
GOTERM_BP_FA_T	GO:0031333~negative regulation of protein complex assembly	4	2.81690141	9.38E-04
GOTERM_BP_FA_T	GO:0032970~regulation of actin filament-based process	5	3.52112676	9.69E-04
GOTERM_MF_FA_T	GO:0003779~actin binding	9	6.33802817	0.00200343

GOTERM_BP_FA_T	GO:0030833~regulation of actin filament polymerization	4	2.81690141	0.00414527
GOTERM_BP_FA_T	GO:0051494~negative regulation of cytoskeleton organization	4	2.81690141	0.00497456
GOTERM_BP_FA_T	GO:0008064~regulation of actin polymerization or depolymerization	4	2.81690141	0.00557906
GOTERM_BP_FA_T	GO:0030832~regulation of actin filament length	4	2.81690141	0.00589711
GOTERM_BP_FA_T	GO:0051693~actin filament capping	3	2.11267606	0.00812838
GOTERM_BP_FA_T	GO:0030835~negative regulation of actin filament depolymerization	3	2.11267606	0.00988929
GOTERM_BP_FA_T	GO:0010639~negative regulation of organelle organization	4	2.81690141	0.01011725
GOTERM_BP_FA_T	GO:0030834~regulation of actin filament depolymerization	3	2.11267606	0.01281651
GOTERM_BP_FA_T	GO:0043242~negative regulation of protein complex disassembly	3	2.11267606	0.02625146
GOTERM_BP_FA_T	GO:0032535~regulation of cellular component size	5	3.52112676	0.02906941
GOTERM_BP_FA_T	GO:0043244~regulation of protein complex disassembly	3	2.11267606	0.03839267

Annotation Cluster 10	Enrichment Score: 2.7548487952127245			
Category	Term	Count	%	PValue
GOTERM_BP_FA_T	GO:0051270~regulation of cell motion	6	4.22535211	0.00104751
GOTERM_BP_FA_T	GO:0040012~regulation of locomotion	6	4.22535211	0.00118569
GOTERM_BP_FA_T	GO:0030334~regulation of cell migration	5	3.52112676	0.0043785

Annotation Cluster 11	Enrichment Score: 2.449430586988362			
Category	Term	Count	%	PValue
GOTERM_CC_FA_T	GO:0016323~basolateral plasma membrane	9	6.33802817	2.73E-05
GOTERM_CC_FA_T	GO:0009925~basal plasma membrane	5	3.52112676	1.02E-04
GOTERM_CC_FA_T	GO:0045178~basal part of cell	5	3.52112676	1.17E-04

GOTERM_CC_FA T	GO:0045177~apical part of cell	6	4.22535211	0.00620078
GOTERM_CC_FA T	GO:0016324~apical plasma membrane	5	3.52112676	0.01024807
GOTERM_CC_FA T	GO:0031226~intrinsic to plasma membrane	6	4.22535211	0.51331246
GOTERM_CC_FA T	GO:0005887~integral to plasma membrane	5	3.52112676	0.67172268

Annotation Cluster 12	Enrichment Score: 2.184089126642428	Count	%	PValue
Category	Term	Count	%	PValue
GOTERM_BP_FA T	GO:0051493~regulation of cytoskeleton organization	7	4.92957746	7.87E-05
GOTERM_BP_FA T	GO:0033043~regulation of organelle organization	7	4.92957746	8.58E-04
GOTERM_BP_FA T	GO:0051495~positive regulation of cytoskeleton organization	3	2.11267606	0.01495179
GOTERM_BP_FA T	GO:0010638~positive regulation of organelle organization	3	2.11267606	0.0540888
GOTERM_BP_FA T	GO:0051130~positive regulation of cellular component organization	3	2.11267606	0.2197952

Annotation Cluster 13	Enrichment Score: 2.0841120208176855	Count	%	PValue
Category	Term	Count	%	PValue
GOTERM_CC_FA T	GO:0005912~adherens junction	6	4.22535211	0.002135
GOTERM_CC_FA T	GO:0005913~cell-cell adherens junction	4	2.81690141	0.00230052
GOTERM_CC_FA T	GO:0070161~anchoring junction	6	4.22535211	0.00406102
GOTERM_BP_FA T	GO:0007163~establishment or maintenance of cell polarity	3	2.11267606	0.02090042
GOTERM_BP_FA T	GO:0016337~cell-cell adhesion	5	3.52112676	0.09108038

Annotation Cluster 14	Enrichment Score: 1.94341292571509	Count	%	PValue
Category	Term	Count	%	PValue
GOTERM_MF_FA T	GO:0008092~cytoskeletal protein binding	13	9.15492958	1.02E-04
GOTERM_CC_FA T	GO:0015629~actin cytoskeleton	8	5.63380282	0.00187887

GOTERM_CC_FA T	GO:0005856~cytoskeleton	19	13.3802817	0.00664539
GOTERM_CC_FA T	GO:0043232~intracellular non-membrane-bounded organelle	23	16.1971831	0.08910709
GOTERM_CC_FA T	GO:0043228~non-membrane-bounded organelle	23	16.1971831	0.08910709
GOTERM_CC_FA T	GO:0044430~cytoskeletal part	10	7.04225352	0.21702765

Annotation Cluster 15	Enrichment Score: 1.9299502648276492	Count	%	PValue
Category	Term	Count	%	PValue
GOTERM_BP_FA T	GO:0001936~regulation of endothelial cell proliferation	4	2.81690141	4.40E-04
GOTERM_CC_FA T	GO:0045121~membrane raft	6	4.22535211	7.96E-04
GOTERM_BP_FA T	GO:0006461~protein complex assembly	8	5.63380282	0.00126372
GOTERM_BP_FA T	GO:0070271~protein complex biogenesis	8	5.63380282	0.00126372
GOTERM_BP_FA T	GO:0001937~negative regulation of endothelial cell proliferation	3	2.11267606	0.00324195
GOTERM_BP_FA T	GO:0065003~macromolecular complex assembly	8	5.63380282	0.01110494
GOTERM_BP_FA T	GO:0043933~macromolecular complex subunit organization	8	5.63380282	0.01679594
GOTERM_BP_FA T	GO:0008285~negative regulation of cell proliferation	5	3.52112676	0.07865318
GOTERM_BP_FA T	GO:0043623~cellular protein complex assembly	3	2.11267606	0.18303415
GOTERM_BP_FA T	GO:0034621~cellular macromolecular complex subunit organization	4	2.81690141	0.2597371
GOTERM_BP_FA T	GO:0034622~cellular macromolecular complex assembly	3	2.11267606	0.46585214



Genes	List Total	Pop Hits
COL4A4, COL4A3, COL4A2, COL4A1, NPNT, DAG1, SPARC, TIMP3, LAMA5, VEGFA, LAMC2, LAMC1, AGRN	108	73
COL4A4, COL4A3, COL4A2, COL4A1, NPNT, DAG1, SPARC, TIMP3, LAMA5, VEGFA, LAMC2, LAMC1, AGRN	108	92
COL4A4, COL4A3, COL4A2, COL4A1, LGALS3, NPNT, DAG1, SPARC, MMP14, TIMP3, A930038C07RIK, LAMA5, VEGFA, LAMC2, LAMC1, AGRN	108	309
COL4A4, COL4A3, COL4A2, COL4A1, LGALS3, NPNT, DAG1, SPARC, MMP14, TIMP3, LAMA5, VEGFA, LAMC2, LAMC1, AGRN	108	297
COL4A4, COL4A3, COL4A2, COL4A1, LGALS3, NPNT, DAG1, SPARC, MMP14, AGER, TIMP3, A930038C07RIK, LAMA5, VEGFA, LAMC2, AGRN, LAMC1, ADAM9	108	774
EDN3, PXdN, NPNT, IGFBP7, IGFBP6, DAG1, TIMP3, A930038C07RIK, GSN, MSLN, AGRN, SEMA3A, ADAM9, COL4A4, COL4A3, COL4A2, COL4A1, LGALS3, SPARC, TINAGL1, MMP14, AGER, LAMA5, FBLN5, VEGFA, TMSB4X, LAMC2, LAMC1	108	1680

Genes	List Total	Pop Hits
COL4A4, COL4A3, COL4A2, COL4A1	108	6
COL4A4, COL4A3, COL4A2, COL4A1	108	6
COL4A4, COL4A3, COL4A2, COL4A1, LAMC1	106	30
COL4A4, COL4A3, COL4A2, COL4A1	108	19

Genes	List Total	Pop Hits
EGFR, EDN3, PDPN, PODXL, GJA1, MMP14, MYH9, CD9, CTTNBP2, LAMA5, VEGFA, LAMC1, SEMA3A	99	367
EGFR, CTTNBP2, EDN3, LAMA5, PODXL, VEGFA, GJA1, LAMC1, MYH9, MMP14	99	240
EGFR, CTTNBP2, EDN3, LAMA5, PODXL, VEGFA, GJA1, LAMC1, MYH9, MMP14	99	284
EGFR, CTTNBP2, EDN3, LAMA5, PODXL, VEGFA, GJA1, LAMC1, MYH9, MMP14	99	284

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Genes	List Total	Pop Hits
MYL6, CTTNBP2, GSN, LIMCH1, RHOA, TMSB4X, CNN2, MYH9, EHD2, AKAP2	99	176
CTTNBP2, GSN, LIMCH1, RHOA, TMSB4X, CNN2, MYH9, EHD2, AKAP2	99	165
MYO1C, LMO7, CTNNA1, MYH9, CTTNBP2, GSN, SPNB2, LIMCH1, TMOD3, CNN2, TMSB4X, MTAP6, MSN	106	414
MYO1C, GSN, LIMCH1, SPNB2, TMOD3, TMSB4X, CNN2, MYH9, CTNNA1	106	288
CTTNBP2, GSN, LIMCH1, RHOA, TMSB4X, CNN2, MYH9, EHD2, AKAP2	99	326

Genes	List Total	Pop Hits
PARD6B, MAGI3, TJP1, CLDN18, MAGI1, MPP5, LMO7, GJA1, MYH9, CTNNA1, AHNAK	108	173
PARD6B, MAGI3, TJP1, CLDN18, MAGI1, MPP5, CTNNA1	108	101
PARD6B, MAGI3, TJP1, CLDN18, MAGI1, MPP5, CTNNA1	108	103
PARD6B, MAGI3, TJP1, CLDN18, MAGI1, MPP5	108	76
PARD6B, MAGI3, TJP1, CLDN18, MAGI1, MPP5	108	76
PARD6B, CLDN18, LIMS1, MAGI3, MAGI1, MPP5, LMO7, GJA1, CTNNA1, MYH9, CTTNBP2, TJP1, AHNAK	108	470

Genes	List Total	Pop Hits
CTTNBP2, PDPN, LAMA5, WWP1, ANO1, VEGFA, HOPX, DAG1, CUX1, MMP14	99	124
CTTNBP2, PDPN, LAMA5, WWP1, VEGFA, HOPX, DAG1, CUX1, MMP14	99	111
CTTNBP2, PDPN, LAMA5, WWP1, VEGFA, HOPX, DAG1, CUX1, MMP14	99	113
CTTNBP2, PDPN, LAMA5, NPNT, WWP1, VEGFA, HOPX, DAG1, GJA1, CUX1, MMP14	99	264
EGFR, LAMA5, DAG1, SEMA3A	99	27
EGFR, LAMA5, DAG1, SEMA3A	99	31
PDPN, LAMA5, NPNT, VEGFA, DAG1, GJA1, MMP14	99	171

LAMA5, NPNT, VEGFA, DAG1, SEMA3A, MMP14	99	125
EGFR, CTTNBP2, CAV1, LAMA5, VEGFA, DAG1, SEMA3A	99	197
EGFR, CAV1, LAMA5, DAG1, SEMA3A	99	84
EGFR, LAMA5, DAG1, SEMA3A	99	41
EGFR, LAMA5, NPNT, VEGFA, DAG1, GJA1, SEMA3A, ID3	99	271
LAMA5, NPNT, VEGFA, DAG1, MMP14	99	93
A930038C07RIK, LAMA5, NPNT, PODXL, MMP14	99	94
LAMA5, DAG1, SEMA3A	99	18
EGFR, LAMA5, NPNT, DAG1, SEMA3A	99	173
EGFR, LAMA5, NPNT, DAG1, SEMA3A	99	238
LAMA5, NPNT, DAG1	99	111

Genes	List Total	Pop Hits
MYL6, CAV2, CAV1, RHOA, PPP3CA, AGRN, F2R	99	72
MYL6, CAV2, CAV1, RHOA, PPP3CA, AGRN, F2R	99	74
MYL6, CAV2, CAV1, CRYAB, LAMA5, RHOA, PPP3CA, AGRN, F2R	99	176
MYL6, CAV2, CAV1, RHOA, PPP3CA, AGRN, F2R	99	127
MYL6, CAV2, CAV1, RHOA, PPP3CA, AGRN, F2R	99	136
CAV2, PPP3CA, AGRN, F2R	99	32
CAV2, PPP3CA, AGRN, MYH9, QK, F2R	99	117
CAV2, PPP3CA, AGRN, F2R	99	38
CAV2, PPP3CA, AGRN, MYH9, F2R	99	89
CAV2, PPP3CA, AGRN, F2R	99	54

CAV2, PPP3CA, AGRN, F2R	99	61
AGRN, MYH9, F2R	108	319

Genes	List Total	Pop Hits
EGFR, CD9, LIMS1, PDPN, LAMA5, CLIC5, RHOA, SEMA3A, MYH9, PMP22, WWTR1, CTNNA1	99	351
EGFR, LIMS1, PDPN, LAMA5, CLIC5, RHOA, SEMA3A, MYH9, WWTR1, CTNNA1	99	309
LAMA5, PRDX6, CLIC5, SEMA3A, MYH9, WWTR1	99	319

Genes	List Total	Pop Hits
CTTNBP2, CAV1, GSN, SPNB2, RHOA, TMOD3, TMSB4X, AGRN, MMP14	99	89
CTTNBP2, CAV1, GSN, SPNB2, TMOD3, TMSB4X	99	57
CTTNBP2, CAV1, GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	99
CTTNBP2, CAV1, GSN, SPNB2, TMOD3, TMSB4X	99	65
GSN, SPNB2, TMOD3, TMSB4X, SEMA3A, MMP14	99	93
GSN, SPNB2, TMOD3, TMSB4X	99	25
CTTNBP2, CAV1, GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	154
GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	60
GSN, SPNB2, TMOD3, TMSB4X	99	27
GSN, SPNB2, TMOD3, TMSB4X	99	27
GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	61
MYO1C, GSN, LIMCH1, SPNB2, TMOD3, TMSB4X, CNN2, MYH9, CTNNA1	106	288

GSN, SPNB2, TMOD3, TMSB4X	99	45
GSN, SPNB2, TMOD3, TMSB4X	99	48
GSN, SPNB2, TMOD3, TMSB4X	99	50
GSN, SPNB2, TMOD3, TMSB4X	99	51
GSN, SPNB2, TMOD3	99	19
GSN, SPNB2, TMOD3	99	21
GSN, SPNB2, TMOD3, TMSB4X	99	62
GSN, SPNB2, TMOD3	99	24
GSN, SPNB2, TMOD3	99	35
GSN, SPNB2, TMOD3, TMSB4X, SEMA3A	99	161
GSN, SPNB2, TMOD3	99	43

Genes	List Total	Pop Hits
EDN3, PDPN, LAMA5, TMOD3, TMSB4X, SEMA3A	99	107
EDN3, PDPN, LAMA5, TMSB4X, SEMA3A, AGER	99	110
EDN3, PDPN, LAMA5, TMSB4X, SEMA3A	99	92

Genes	List Total	Pop Hits
EGFR, CTTNBP2, LIMS1, TJP1, CAV1, AQP5, SLC03A1, MSN, AGER	108	141
CTTNBP2, CAV1, AQP5, SLC03A1, AGER	108	29
CTTNBP2, CAV1, AQP5, SLC03A1, AGER	108	30

PARD6B, CTTNBP2, AQP5, LMO7, SLC03A1, MSN	108	136
CTTNBP2, AQP5, LMO7, SLC03A1, MSN	108	99
CAV2, CAV1, ITGB6, AQP5, SLC03A1, ADAM9	108	552
CAV2, CAV1, ITGB6, AQP5, SLC03A1	108	531

Genes	List Total	Pop Hits
CTTNBP2, CAV1, GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	99
CTTNBP2, CAV1, GSN, SPNB2, RHOA, TMOD3, TMSB4X	99	154
CTTNBP2, CAV1, RHOA	99	26
CTTNBP2, CAV1, RHOA	99	52
CTTNBP2, CAV1, RHOA	99	122

Genes	List Total	Pop Hits
CTTNBP2, LIMS1, TJP1, LMO7, MYH9, CTNNA1	108	106
TJP1, LMO7, MYH9, CTNNA1	108	31
CTTNBP2, LIMS1, TJP1, LMO7, MYH9, CTNNA1	108	123
LIMS1, MYH9, CTNNA1	99	31
LIMS1, CLDN18, PDPN, LMO7, MYH9	99	236

Genes	List Total	Pop Hits
MYO1C, LMO7, CTNNA1, MYH9, CTTNBP2, GSN, SPNB2, LIMCH1, TMOD3, CNN2, TMSB4X, MTAP6, MSN	106	414
MYL6, CTTNBP2, MYO1C, SPNB2, CLIC5, TMOD3, MYH9, CTNNA1	108	205

MYL6, ACTB, MYO1C, 1190002H23RIK, DAG1, MYH9, CTNNA1, CTTNBP2, KRT19, FRMD6, GSN, SPNB2, KRT7, CLIC5, RHOA, TMOD3, MTAP6, TMSB4X, MSN	108	1122
MYL6, ACTB, MYO1C, XIST, 1190002H23RIK, DAG1, MYH9, CTNNA1, CTTNBP2, KRT19, FRMD6, RPS19, MRPL14, GSN, CLIC5, KRT7, SPNB2, RHOA, TMOD3, MTAP6, TMSB4X, MSN, 2200002D01RIK	108	1919
MYL6, ACTB, MYO1C, XIST, 1190002H23RIK, DAG1, MYH9, CTNNA1, CTTNBP2, KRT19, FRMD6, RPS19, MRPL14, GSN, CLIC5, KRT7, SPNB2, RHOA, TMOD3, MTAP6, TMSB4X, MSN, 2200002D01RIK	108	1919
MYL6, KRT19, MYO1C, SPNB2, CLIC5, KRT7, 1190002H23RIK, TMOD3, MTAP6, MYH9	108	774

Genes	List Total	Pop Hits
CTTNBP2, CAV2, CAV1, VEGFA	99	21
CTTNBP2, CAV2, CAV1, PTRF, SDPR, DAG1	108	85
PARD6B, CTTNBP2, CAV2, CAV1, PTRF, GSN, LAMC1, AGRN	99	227
PARD6B, CTTNBP2, CAV2, CAV1, PTRF, GSN, LAMC1, AGRN	99	227
CTTNBP2, CAV2, CAV1	99	12
PARD6B, CTTNBP2, CAV2, CAV1, PTRF, GSN, LAMC1, AGRN	99	338
PARD6B, CTTNBP2, CAV2, CAV1, PTRF, GSN, LAMC1, AGRN	99	367
CD9, CTTNBP2, CAV2, CAV1, CTNNA1	99	224
CTTNBP2, GSN, AGRN	99	108
CTTNBP2, PTRF, GSN, AGRN	99	245
CTTNBP2, GSN, AGRN	99	217

[REDACTED]

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
12504	20.6179604	1.92E-10	1.92E-10	1.22E-09
12504	16.3599034	3.32E-09	1.66E-09	2.11E-08
12504	5.99496584	1.07E-05	3.56E-06	6.78E-05
12504	5.84736251	4.42E-05	1.10E-05	2.80E-04
12504	2.69250646	0.055724	0.00408713	0.36323822
12504	1.92962963	0.13506	0.00802843	0.91664338

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
12504	77.1851852	0.002353	2.94E-04	0.01495191
12504	77.1851852	0.002353	2.94E-04	0.01495191
13288	20.8930818	0.020374	0.0102395	0.11103432
12504	24.374269	0.099932	0.00655872	0.66598261

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	4.86180607	0.012584	0.00158178	0.01998976
13588	5.71885522	0.056227	0.00361029	0.09131023
13588	4.8328354	0.187682	0.01088054	0.32759365
13588	4.8328354	0.187682	0.01088054	0.32759365

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	7.79843893	0.004888	7.00E-04	0.00773507
13588	7.48650138	0.024557	0.00206985	0.03924229
13288	3.93637772	0.023984	0.00805953	0.13093604
13288	3.91745283	0.380783	0.09140878	2.55363609
13588	3.78918015	0.913164	0.05524633	3.78420503

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
12504	7.36159281	4.31E-04	7.19E-05	0.00273784
12504	8.02420242	0.043131	0.00366729	0.27942343
12504	7.86839266	0.047877	0.00376682	0.31089019
12504	9.14035088	0.089611	0.00623935	0.59407536
12504	9.14035088	0.089611	0.00623935	0.59407536
12504	3.20236407	0.123832	0.00774615	0.83550263

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	11.068752	2.61E-04	1.30E-04	4.12E-04
13588	11.1285831	0.001315	4.39E-04	0.00207774
13588	10.9316171	0.001506	3.77E-04	0.00237979
13588	5.71885522	0.01997	0.00183217	0.03183881
13588	20.3337074	0.609297	0.02986146	1.47262439
13588	17.7100033	0.757014	0.03853653	2.20856703
13588	5.61852443	0.771434	0.0391049	2.30296353

13588	6.58812121	0.876531	0.04858405	3.2481251
13588	4.87699328	0.95067	0.06332423	4.63929123
13588	8.16979317	0.957864	0.06516017	4.87628736
13588	13.3904903	0.958734	0.06425348	4.90758798
13588	4.05173506	0.968027	0.06653987	5.28981469
13588	7.37916802	0.989593	0.08106786	6.95322756
13588	7.30066624	0.991285	0.08261739	7.21338069
13588	22.8754209	0.999352	0.10836985	10.9422648
13588	3.96683599	1	0.31549571	44.368171
13588	2.88345641	1	0.54047904	78.7031292
13588	3.70952771	1	0.74079006	96.4779233

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	13.3439955	0.012765	0.00142643	0.02027815
13588	12.983347	0.014944	0.00150456	0.02376598
13588	7.01859504	0.038712	0.00303243	0.06230576
13588	7.56509982	0.265986	0.01534244	0.48695428
13588	7.06446821	0.36002	0.0192181	0.70207987
13588	17.1565657	0.788408	0.04004698	2.42189687
13588	7.03859104	0.790492	0.03928426	2.43713932
13588	14.4476342	0.922813	0.05533306	3.96295028
13588	7.71081603	0.979774	0.07363398	5.97198819
13588	10.1668537	0.999038	0.1044007	10.3858799

13588	9.00016559	0.999941	0.13157886	14.2442367
12504	1.08881923	1	0.98030341	99.9999984

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	4.69239403	0.043041	0.00313757	0.06942629
13588	4.4418293	0.321057	0.01826998	0.60939505
13588	2.5815522	1	0.50454234	73.5608743

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	13.8794688	2.40E-04	2.40E-04	3.78E-04
13588	14.4476342	0.053369	0.00364974	0.08654254
13588	9.70472401	0.075774	0.00462447	0.12431335
13588	12.6694639	0.09822	0.00572714	0.16306947
13588	8.85500163	0.425952	0.02195705	0.87235888
13588	21.960404	0.526064	0.02631481	1.17178897
13588	6.23875115	0.576663	0.02920595	1.34777408
13588	11.4377104	0.598231	0.02993866	1.42917558
13588	20.3337074	0.609297	0.02986146	1.47262439
13588	20.3337074	0.609297	0.02986146	1.47262439
13588	11.250207	0.621126	0.02987439	1.5204291
13288	3.91745283	0.380783	0.09140878	2.55363609

13588	12.2002245	0.984362	0.0768489	6.35307551
13588	11.4377104	0.993208	0.08528449	7.57778421
13588	10.980202	0.996303	0.09055424	8.4610476
13588	10.7649039	0.997316	0.09249572	8.9225809
13588	21.6714514	0.999717	0.11642956	12.0997334
13588	19.6075036	0.999952	0.13248349	14.533495
13588	8.85500163	0.999962	0.13356265	14.8439088
13588	17.1565657	0.999998	0.15624916	18.4400613
13588	11.7645022	1	0.26367078	34.3189868
13588	4.26250078	1	0.28236593	37.2590325
13588	9.57575758	1	0.32688615	46.1314356

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	7.69640329	0.649748	0.03129096	1.64246861
13588	7.48650138	0.695042	0.03432588	1.85724467
13588	7.45937637	0.98763	0.07953607	6.69904327

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
12504	7.39007092	0.005363	5.97E-04	0.03412033
12504	19.9616858	0.019912	0.00200925	0.12756747
12504	19.2962963	0.022791	0.00209372	0.14621561

12504	5.10784314	0.706347	0.04281896	7.48221849
12504	5.84736251	0.868571	0.06336426	12.0843255
12504	1.25845411	1	0.89102745	99.9877056
12504	1.09018623	1	0.96219025	99.9999105

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	9.70472401	0.075774	0.00462447	0.12431335
13588	6.23875115	0.576663	0.02920595	1.34777408
13588	15.8368298	1	0.17377074	21.1835211
13588	7.91841492	1	0.39990201	58.4669173
13588	3.3750621	1	0.78017444	98.0197942

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
12504	6.55345912	0.34364	0.01813978	2.6368477
12504	14.9390681	0.364743	0.01872762	2.83857572
12504	5.64769648	0.551412	0.03036221	4.96054557
13588	13.2825024	1	0.22487852	28.3776367
13588	2.90789248	1	0.53741282	77.8878432

Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13288	3.93637772	0.023984	0.00805953	0.13093604
12504	4.51815718	0.3096	0.0166992	2.32391474

12504	1.96058625	0.731125	0.04428303	7.9983965
12504	1.38764403	1	0.31286496	68.8669017
12504	1.38764403	1	0.31286496	68.8669017
12504	1.49583692	1	0.59722967	95.3062727
Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
13588	26.1433381	0.356501	0.0198385	0.6934826
12504	8.17254902	0.145197	0.00781354	0.99075416
13588	4.8370934	0.717983	0.03551917	1.97833136
13588	4.8370934	0.717983	0.03551917	1.97833136
13588	34.3131313	0.961244	0.06418352	5.00173325
13588	3.24858048	0.999986	0.14197872	16.1766665
13588	2.99188066	1	0.18887052	23.483134
13588	3.06367244	1	0.50088607	72.5953475
13588	3.81257015	1	0.72897639	95.9010718
13588	2.24085756	1	0.81922732	99.1368755
13588	1.89750035	1	0.95665432	99.9950274



Category	Term	Count	%	PValue
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	5	3.401360544	0.002424239
KEGG_PATHWAY	mmu03320:PPAR signaling pathway	5	3.401360544	0.004409337
KEGG_PATHWAY	mmu04142:Lysosome	4	2.721088435	0.080563269

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
CD36, STK11, PPARGC1A, IRS1, ACSL5	50	67	5738	8.564179104	0.164405222
SCD1, CD36, DBI, FABP5, ACSL5	50	79	5738	7.263291139	0.278925206
NPC1, LAMP3, CTSC, NAPSA	50	119	5738	3.857478992	0.998001902

Benjamini	FDR
0.164405222	2.508458161
0.15083877	4.519982669
0.874047838	58.48600141

Annotation Cluster 1	Enrichment Score: 4.113345490182897			
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0044421~extracellular region part	18	12.24489796	3.65E-05
GOTERM_CC_FAT	GO:0005576~extracellular region	28	19.04761905	3.94E-05
GOTERM_CC_FAT	GO:0005615~extracellular space	13	8.843537415	3.18E-04

Annotation Cluster 2	Enrichment Score: 2.5709486581195917			
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0044421~extracellular region part	18	12.24489796	3.65E-05
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	7	4.761904762	0.021144241
GOTERM_CC_FAT	GO:0031012~extracellular matrix	7	4.761904762	0.025091643

Annotation Cluster 3	Enrichment Score: 2.5535027937954005			
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0005764~lysosome	8	5.442176871	3.12E-04
GOTERM_CC_FAT	GO:0000323~lytic vacuole	8	5.442176871	3.22E-04
GOTERM_CC_FAT	GO:0005773~vacuole	8	5.442176871	7.06E-04
GOTERM_BP_FAT	GO:0046907~intracellular transport	3	2.040816327	0.86142551

Annotation Cluster 4	Enrichment Score: 1.8027112454950656			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	6	4.081632653	0.009195766

GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	4	2.721088435	0.018188779
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	4	2.721088435	0.023360105

Annotation Cluster 5	Enrichment Score: 1.6977202560266051			
Category	Term	Count	%	PValue
GOTERM_MF_FAT	GO:0004864~phosphoprotein phosphatase inhibitor activity	3	2.040816327	0.011103901
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	7	4.761904762	0.013719792
GOTERM_MF_FAT	GO:0019212~phosphatase inhibitor activity	3	2.040816327	0.014555941
GOTERM_MF_FAT	GO:0019888~protein phosphatase regulator activity	3	2.040816327	0.035630482
GOTERM_MF_FAT	GO:0019208~phosphatase regulator activity	3	2.040816327	0.04108787

Annotation Cluster 6	Enrichment Score: 1.2187937458853346			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0015918~sterol transport	3	2.040816327	0.014202835
GOTERM_BP_FAT	GO:0030301~cholesterol transport	3	2.040816327	0.014202835
GOTERM_BP_FAT	GO:0006869~lipid transport	3	2.040816327	0.244139751
GOTERM_BP_FAT	GO:0010876~lipid localization	3	2.040816327	0.270667685

Annotation Cluster 7	Enrichment Score: 1.162344901431801			
Category	Term	Count	%	PValue
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	7	4.761904762	0.013719792
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	4	2.721088435	0.140406225
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	4	2.721088435	0.169134192

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
CSF2, HC, EGFL6, CHI3L1, IL33, SFTPA1, ARG1, SERPINF1, CXCL15, PON1, SFTPB, COL6A2, CMTM8, SFTPC, ADAMTS1, ADAM19, TECTB, SFTPB	92	774	12504	3.1607685
FGFR2, RETNLA, GALNT2, CSF2, EPDR1, SFTPA1, IL33, ARG1, PLA2G1B, COL6A2, SFTPB, SFTPC, LGI3, TECTB, SFTPB, DPP4, RNASE4, HC, EGFL6, CHI3L1, GIF, LCN2, SERPINF1, CXCL15, PON1, CMTM8, ADAMTS1, ADAM19	92	1680	12504	2.2652174
CSF2, HC, CHI3L1, SFTPA1, IL33, ARG1, SERPINF1, CXCL15, SFTPB, CMTM8, PON1, SFTPC, SFTPB	92	511	12504	3.4576704

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
CSF2, HC, EGFL6, CHI3L1, IL33, SFTPA1, ARG1, SERPINF1, CXCL15, PON1, SFTPB, COL6A2, CMTM8, SFTPC, ADAMTS1, ADAM19, TECTB, SFTPB	92	774	12504	3.1607685
EGFL6, COL6A2, SFTPB, ADAMTS1, ADAM19, SFTPA1, TECTB	92	297	12504	3.2033377
EGFL6, COL6A2, SFTPB, ADAMTS1, ADAM19, SFTPA1, TECTB	92	309	12504	3.0789363

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
NPC1, LAMP3, EPDR1, CTSC, DRAM1, CD74, SFTPB, RAB27A	92	178	12504	6.1084514
NPC1, LAMP3, EPDR1, CTSC, DRAM1, CD74, SFTPB, RAB27A	92	179	12504	6.074326
NPC1, LAMP3, EPDR1, CTSC, DRAM1, CD74, SFTPB, RAB27A	92	204	12504	5.3299233
NPC1, CD74, RAB27A	109	431	13588	0.8677068

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
SOAT1, NPC1, HSD3B7, PON1, CFTR, CAT	109	161	13588	4.6457348

SOAT1, PON1, CFTR, CAT	109	70	13588	7.12346
SOAT1, PON1, CFTR, CAT	109	77	13588	6.4758728

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
PPP1R8, PPP1R1A, PPP1R14C	108	20	13288	18.455556
BCL2A1D, SERPINF1, HC, PPP1R8, PPP1R1A, ITIH4, PPP1R14C	108	243	13288	3.5442768
PPP1R8, PPP1R1A, PPP1R14C	108	23	13288	16.048309
PPP1R8, PPP1R1A, PPP1R14C	108	37	13288	9.975976
PPP1R8, PPP1R1A, PPP1R14C	108	40	13288	9.2277778

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
NPC1, CD36, CFTR	109	23	13588	16.260072
NPC1, CD36, CFTR	109	23	13588	16.260072
NPC1, CD36, CFTR	109	119	13588	3.142703
NPC1, CD36, CFTR	109	128	13588	2.9217317

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
BCL2A1D, SERPINF1, HC, PPP1R8, PPP1R1A, ITIH4, PPP1R14C	108	243	13288	3.5442768
BCL2A1D, SERPINF1, HC, ITIH4	108	161	13288	3.0568208
BCL2A1D, SERPINF1, HC, ITIH4	108	176	13288	2.7962963

Bonferroni	Benjamini	FDR
0.00561	0.005607	0.0437908
0.00605	0.003031	0.0472765
0.04774	0.012154	0.3802828

Bonferroni	Benjamini	FDR
0.00561	0.005607	0.0437908
0.96279	0.375099	22.61417
0.98003	0.352622	26.275886

Bonferroni	Benjamini	FDR
0.04687	0.015873	0.3732204
0.04845	0.009884	0.3861156
0.10302	0.017957	0.8433359
1	0.999999	100

Bonferroni	Benjamini	FDR
0.99968	0.982106	13.358569

1	0.959142	24.792222
1	0.947195	30.711078

Bonferroni	Benjamini	FDR
0.96896	0.968965	13.931851
0.98638	0.883306	16.941137
0.98954	0.7813	17.882297
0.99999	0.895301	38.5829
1	0.886359	43.092021

Bonferroni	Benjamini	FDR
1	0.984285	19.910808
1	0.984285	19.910808
1	0.998625	98.702121
1	0.998563	99.254578

Bonferroni	Benjamini	FDR
0.98638	0.883306	16.941137
1	0.904883	86.903985
1	0.927145	91.705576

Annotation Cluster 1	Enrichment Score: 1.5978270030440043			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	7	4.827586207	0.013326757
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	8	5.517241379	0.033998125
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	8	5.517241379	0.035509089
Annotation Cluster 2	Enrichment Score: 1.5911320361877224			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	7	4.827586207	0.00307928
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	3	2.068965517	0.051351715
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	3	2.068965517	0.051351715
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	3	2.068965517	0.053200134
Annotation Cluster 3	Enrichment Score: 1.2073045814383705			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependent	8	5.517241379	0.007232238
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	8	5.517241379	0.007482697
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	9	6.206896552	0.011233258
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	9	6.206896552	0.013150379
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	7	4.827586207	0.013326757
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	9	6.206896552	0.013839965
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	8	5.517241379	0.01888245
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	8	5.517241379	0.025833815

GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	6	4.137931034	0.026807386
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	8	5.517241379	0.027089721
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	8	5.517241379	0.030067059
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	9	6.206896552	0.03123497
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	8	5.517241379	0.162157745
GOTERM_MF_FAT	GO:0003677~DNA binding	17	11.72413793	0.175250987
GOTERM_BP_FAT	GO:0006350~transcription	17	11.72413793	0.21458267
GOTERM_BP_FAT	GO:0045449~regulation of transcription	20	13.79310345	0.261683321
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	14	9.655172414	0.26728716
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	14	9.655172414	0.285982725
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	6	4.137931034	0.349348533
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	3	2.068965517	0.436198153
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	10	6.896551724	0.471743834
GOTERM_MF_FAT	GO:0003700~transcription factor activity	6	4.137931034	0.639280088
Annotation Cluster 4	Enrichment Score: 1.1459537354669358			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	7	4.827586207	0.00307928

GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	4	2.75862069	0.084000847
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduction	5	3.448275862	0.085102054
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	6	4.137931034	0.108913939
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	6	4.137931034	0.11465013
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	3	2.068965517	0.115383126
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	4	2.75862069	0.145559903
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	3	2.068965517	0.147249935
Annotation Cluster 5	Enrichment Score: 1.1037585154494782			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0051674~localization of cell	6	4.137931034	0.05646624
GOTERM_BP_FAT	GO:0048870~cell motility	6	4.137931034	0.05646624
GOTERM_CC_FAT	GO:0042995~cell projection	8	5.517241379	0.074552939
GOTERM_BP_FAT	GO:0016477~cell migration	5	3.448275862	0.098137822
GOTERM_BP_FAT	GO:0006928~cell motion	6	4.137931034	0.12981608
Annotation Cluster 6	Enrichment Score: 1.0983228677980152			
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	4	2.75862069	0.028240205
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	4	2.75862069	0.042411186
GOTERM_CC_FAT	GO:0000790~nuclear chromatin	3	2.068965517	0.048263886
GOTERM_CC_FAT	GO:0044427~chromosomal part	6	4.137931034	0.052878393
GOTERM_CC_FAT	GO:0000785~chromatin	4	2.75862069	0.089001761
GOTERM_CC_FAT	GO:0005694~chromosome	6	4.137931034	0.094441456
GOTERM_BP_FAT	GO:0051276~chromosome organization	3	2.068965517	0.79786581

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
CEBPA, SMARCB1, GABPA, MBD3, YBX1, CITED2, SLC34A2	100	267	13588	3.562397
CEBPA, SMARCB1, GABPA, DLK1, MBD3, YBX1, CITED2, SLC34A2	100	421	13588	2.5820428
CEBPA, SMARCB1, GABPA, DLK1, MBD3, YBX1, CITED2, SLC34A2	100	425	13588	2.5577412
Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
BCL2A1D, SPRY1, TBC1D14, MGMT, PTH1R, RICTOR, EIF2AK3	100	196	13588	4.8528571
BCL2A1D, MGMT, EIF2AK3	100	50	13588	8.1528
BCL2A1D, MGMT, EIF2AK3	100	50	13588	8.1528
BCL2A1D, MGMT, EIF2AK3	100	51	13588	7.9929412
Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	308	13588	3.5293506
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	310	13588	3.5065806
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, EIF2AK3, CITED2	100	418	13588	2.9256459
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, EIF2AK3, CITED2	100	430	13588	2.844
CEBPA, SMARCB1, GABPA, MBD3, YBX1, CITED2, SLC34A2	100	267	13588	3.562397
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, EIF2AK3, CITED2	100	434	13588	2.817788
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	372	13588	2.9221505
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	397	13588	2.738136

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3	100	231	13588	3.5293506
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	401	13588	2.7108229
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, CITED2	100	410	13588	2.6513171
CEBPA, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, TRIM24, EIF2AK3, CITED2	100	506	13588	2.4168379
CEBPA, E2F4, RFX5, ZGLP1, GABPA, IRF2BP1, MBD3, CITED2	100	616	13588	1.7646753
CEBPA, LCORL, E2F4, RFX5, GABPA, MGMT, POT1A, TRIM24, MBD3, CIC, XRCC1, YBX1, CITED2, RFC5, RFC3, ZGLP1, ETV5	94	1781	13288	1.3493256
CEBPA, ZFP53, E2F4, LCORL, GABPA, ZFP429, WTIP, IRF2BP1, TRIM24, MBD3, PAWR, CIC, CITED4, YBX1, CITED2, SMARCB1, ZGLP1	100	1772	13588	1.3035892
CEBPA, ZFP53, LCORL, E2F4, RFX5, GABPA, ZFP429, PAWR, WTIP, IRF2BP1, TRIM24, MBD3, CIC, CITED4, YBX1, CITED2, SMARCB1, ZGLP1, 1700048O20RIK, ETV5	100	2227	13588	1.2202964
CEBPA, ZFP53, E2F4, RFX5, GABPA, ZFP429, IRF2BP1, TRIM24, MBD3, YBX1, CITED2, ZGLP1, 1700048O20RIK, ETV5	100	1465	13588	1.2985119
CEBPA, ZFP53, E2F4, RFX5, GABPA, ZFP429, IRF2BP1, TRIM24, MBD3, YBX1, CITED2, ZGLP1, 1700048O20RIK, ETV5	100	1488	13588	1.2784409
CEBPA, ZGLP1, GABPA, POT1A, TRIM24, ETV5	94	556	13288	1.525486
ZGLP1, IRF2BP1, TRIM24	94	211	13288	2.009882
CEBPA, E2F4, LCORL, ZGLP1, GABPA, IRF2BP1, TRIM24, ETV5, CITED4, CITED2	94	1206	13288	1.1721534
CEBPA, E2F4, ZGLP1, GABPA, ETV5, CITED2	94	776	13288	1.0930029
BCL2A1D, SPRY1, TBC1D14, MGMT, PTH1R, RICTOR, EIF2AK3	100	196	13588	4.8528571

ARHGEF7, DOCK7, RICTOR, RIC8B	94	147	13288	3.8465769
SPRY1, ARHGEF7, TBC1D14, SIPA1, RICTOR	100	228	13588	2.9798246
ARHGEF7, TBC1D14, SIPA1, DOCK7, RICTOR, RIC8B	94	361	13288	2.349502
ARHGEF7, TBC1D14, SIPA1, DOCK7, RICTOR, RIC8B	94	367	13288	2.3110905
SPRY1, TBC1D14, RICTOR	100	80	13588	5.0955
SPRY1, ARHGEF7, TBC1D14, RICTOR	100	181	13588	3.0028729
SPRY1, TBC1D14, RICTOR	100	93	13588	4.3832258
Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
SCHIP1, NRP1, CATSPER2, KATNA1, CXCL15, SCARB1	100	284	13588	2.8707042
SCHIP1, NRP1, CATSPER2, KATNA1, CXCL15, SCARB1	100	284	13588	2.8707042
NRP1, CATSPER2, KATNA1, PTH1R, DOCK7, SCARB1, MARK4, SLC34A2	81	575	12504	2.1477617
SCHIP1, NRP1, KATNA1, CXCL15, SCARB1	100	240	13588	2.8308333
SCHIP1, NRP1, CATSPER2, KATNA1, CXCL15, SCARB1	100	367	13588	2.2214714
Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
SMARCB1, POT1A, TRIM24, CITED2	81	103	12504	5.9949658
SMARCB1, POT1A, TRIM24, CITED2	81	121	12504	5.1031527
SMARCB1, TRIM24, CITED2	81	55	12504	8.420202
RFC5, SMARCB1, POT1A, MBD3, TRIM24, CITED2	81	318	12504	2.9126485
SMARCB1, MBD3, TRIM24, CITED2	81	165	12504	3.742312
RFC5, SMARCB1, POT1A, MBD3, TRIM24, CITED2	81	378	12504	2.4503233
SMARCB1, POT1A, MBD3	100	404	13588	1.0090099

Bonferroni	Benjamin i	FDR
0.999996	0.87473	18.94
1	0.86579	41.805
1	0.86134	43.214
Bonferroni	Benjamin i	FDR
0.943021	0.94302	4.7123
1	0.9136	56.181
1	0.9136	56.181
1	0.8795	57.498
Bonferroni	Benjamin i	FDR
0.998821	0.96566	10.739
0.999067	0.9023	11.091
0.999972	0.92747	16.206
0.999995	0.91453	18.713
0.999996	0.87473	18.94
0.999998	0.8427	19.598
1	0.86023	25.797
1	0.89035	33.612

1	0.87799	34.643
1	0.8595	34.939
1	0.86811	37.986
1	0.85989	39.144
1	0.97193	93.728
1	0.99942	91.572
1	0.98309	97.719
1	0.99158	99.133
1	0.99053	99.231
1	0.99248	99.487
1	0.99975	99.598
1	0.99992	99.936
1	0.99983	99.972
1	0.99992	100
Bonferroni	Benjamini	FDR
0.943021	0.94302	4.7123

1	1	67.581
1	0.94771	75.144
1	1	77.246
1	0.99914	79.056
1	0.96491	85.323
1	0.97169	91.474
1	0.9705	91.735
Bonferroni	Benjamini	FDR
1	0.88466	59.736
1	0.88466	59.736
0.999997	0.87813	60.879
1	0.95918	80.144
1	0.96661	88.654
Bonferroni	Benjamini	FDR
0.990622	0.99062	29.32
0.999145	0.97075	40.841
0.999685	0.93196	45.075
0.999857	0.89072	48.216
1	0.85032	67.668
1	0.83415	69.931
1	1	100

Category	Term	Coun t	%	PValue
KEGG_PATHWAY	mmu00980:Metabolism of xenobiotics by cytochrome P450	6	4.081632653	2.45E-04
KEGG_PATHWAY	mmu00982:Drug metabolism	6	4.081632653	4.47E-04
KEGG_PATHWAY	mmu00480:Glutathione metabolism	4	2.721088435	0.010196359
KEGG_PATHWAY	mmu04310:Wnt signaling pathway	5	3.401360544	0.039975011
KEGG_PATHWAY	mmu04110:Cell cycle	4	2.721088435	0.0998346

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
GSTA3, GSTA4, CYP2F2, EPHX1, GSTO1, MGST1	51	66	5738	10.22816399	0.020882
GSTA3, GSTA4, FMO1, FMO2, GSTO1, MGST1	51	75	5738	9.000784314	0.0377
GSTA3, GSTA4, GSTO1, MGST1	51	52	5738	8.654600302	0.585792
CCND1, CCND2, FRAT2, FOSL1, MYC	51	149	5738	3.775496776	0.970057
CCND1, CCND2, SFN, MYC	51	128	5738	3.515931373	0.999882

Benjamini	FDR
0.02088	0.2643
0.01903	0.4807
0.25457	10.463
0.58402	35.591
0.83619	67.831

Annotation Cluster 1	Enrichment Score: 3.046817296355286			
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0005792~microsome	10	6.802721088	1.94E-05
GOTERM_CC_FAT	GO:0042598~vesicular fraction	10	6.802721088	2.53E-05
GOTERM_CC_FAT	GO:0005783~endoplasmic reticulum	18	12.24489796	7.24E-04
GOTERM_CC_FAT	GO:0005624~membrane fraction	12	8.163265306	0.004214984
GOTERM_BP_FAT	GO:0055114~oxidation reduction	13	8.843537415	0.004445567
GOTERM_CC_FAT	GO:0005626~insoluble fraction	12	8.163265306	0.005453864
GOTERM_CC_FAT	GO:0000267~cell fraction	12	8.163265306	0.012928219

Annotation Cluster 2	Enrichment Score: 1.5561278197675796			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0040007~growth	7	4.761904762	0.003310832
GOTERM_BP_FAT	GO:0016049~cell growth	3	2.040816327	0.031337964
GOTERM_BP_FAT	GO:0008361~regulation of cell size	4	2.721088435	0.047626544
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	4	2.721088435	0.120679019

Annotation Cluster 3	Enrichment Score: 1.3806383518810308			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0060429~epithelium development	8	5.442176871	0.004286267
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	6	4.081632653	0.03347651
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	7	4.761904762	0.053169893
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	3	2.040816327	0.116244926
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	4	2.721088435	0.140912334

Annotation Cluster 4	Enrichment Score: 1.3544848171937163			
Category	Term	Coun t	%	PValue
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	9	6.12244898	0.001325444
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	8	5.442176871	0.001477944
GOTERM_BP_FAT	GO:0006954~inflammatory response	7	4.761904762	0.006942838
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	4	2.721088435	0.00853565
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	4	2.721088435	0.00853565
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	4	2.721088435	0.008961449
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	4	2.721088435	0.012814448
GOTERM_BP_FAT	GO:0001818~negative regulation of cytokine production	3	2.040816327	0.013830324
GOTERM_BP_FAT	GO:0009611~response to wounding	8	5.442176871	0.015552757
GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	4	2.721088435	0.015633972
GOTERM_BP_FAT	GO:0002712~regulation of B cell mediated immunity	3	2.040816327	0.021172592
GOTERM_BP_FAT	GO:0002889~regulation of immunoglobulin mediated immune response	3	2.040816327	0.021172592
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	4	2.721088435	0.022242382
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	4	2.721088435	0.022242382
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	5	3.401360544	0.023123438
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	4	2.721088435	0.023720275
GOTERM_BP_FAT	GO:0002250~adaptive immune response	4	2.721088435	0.025250308
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	4	2.721088435	0.025250308

GOTERM_BP_FAT	GO:0002821~positive regulation of adaptive immune response	3	2.040816327	0.026782238
GOTERM_BP_FAT	GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3	2.040816327	0.026782238
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	4	2.721088435	0.028466566
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	5	3.401360544	0.028674802
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	5	3.401360544	0.029872232
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	4	2.721088435	0.033679655
GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	4	2.721088435	0.038376972
GOTERM_BP_FAT	GO:0050868~negative regulation of T cell activation	3	2.040816327	0.039549935
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	4	2.721088435	0.040344818
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	4	2.721088435	0.04236302
GOTERM_BP_FAT	GO:0006952~defense response	8	5.442176871	0.051496357
GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell proliferation	3	2.040816327	0.054152465
GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferation	3	2.040816327	0.054152465
GOTERM_BP_FAT	GO:0051250~negative regulation of lymphocyte activation	3	2.040816327	0.058059498
GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferation	3	2.040816327	0.058059498
GOTERM_BP_FAT	GO:0002695~negative regulation of leukocyte activation	3	2.040816327	0.06004885
GOTERM_BP_FAT	GO:0050866~negative regulation of cell activation	3	2.040816327	0.06004885
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	3	2.040816327	0.064096929
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	3	2.040816327	0.06823451
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	5	3.401360544	0.069413544
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	3	2.040816327	0.081149462
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	4	2.721088435	0.082558724

GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	3	2.040816327	0.085610655
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	4	2.721088435	0.086814032
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	3	2.040816327	0.111364937
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	3	2.040816327	0.111364937
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	3	2.040816327	0.123664816
GOTERM_MF_FAT	GO:0005125~cytokine activity	4	2.721088435	0.141279028
GOTERM_BP_FAT	GO:0006955~immune response	7	4.761904762	0.142870064
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	3	2.040816327	0.143975526
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	4	2.721088435	0.164015033
GOTERM_BP_FAT	GO:0051241~negative regulation of multicellular organismal process	3	2.040816327	0.172917834
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	3	2.040816327	0.194518415
GOTERM_BP_FAT	GO:0002252~immune effector process	3	2.040816327	0.244138919
GOTERM_CC_FAT	GO:0005576~extracellular region	18	12.24489796	0.265604014
GOTERM_CC_FAT	GO:0005615~extracellular space	7	4.761904762	0.272759187
GOTERM_CC_FAT	GO:0044421~extracellular region part	8	5.442176871	0.496288046
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	6	4.081632653	0.518705663

Annotation Cluster 5	Enrichment Score: 1.009610084084379			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0060429~epithelium development	8	5.442176871	0.004286267
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	3	2.040816327	0.368369078
GOTERM_BP_FAT	GO:0035295~tube development	3	2.040816327	0.592662325

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
ACSL1, CYP2F2, PTGS2, FMO1, FMO2, EPHX1, ACSL4, POR, MGST1, IYD	108	176	12504	6.578282828
ACSL1, CYP2F2, PTGS2, FMO1, FMO2, EPHX1, ACSL4, POR, MGST1, IYD	108	182	12504	6.361416361
ACER3, PTGS2, CYP2F2, EPHX1, TMEM132A, FADS2, UPK3A, POR, ACSL1, ATP2A3, FMO1, FMO2, UPK1A, MBOAT1, ACSL4, PPAP2B, RCN1, MGST1	108	838	12504	2.486873508
ACSL1, CYP2F2, PTGS2, FMO1, FMO2, EPHX1, FADS2, ACSL4, CD24A, POR, MGST1, IYD	108	510	12504	2.724183007
LDHB, PTGS2, CYP2F2, FADS2, POR, IYD, ALDH1A1, CBR2, FMO1, FMO2, ALDH1A7, CP, DCXR	103	672	13588	2.552068886
ACSL1, CYP2F2, PTGS2, FMO1, FMO2, EPHX1, FADS2, ACSL4, CD24A, POR, MGST1, IYD	108	528	12504	2.631313131
ACSL1, CYP2F2, PTGS2, FMO1, FMO2, EPHX1, FADS2, ACSL4, CD24A, POR, MGST1, IYD	108	596	12504	2.331096197

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
NOTCH2, HPN, PTGS2, LY6E, MFSD7B, ALKBH1, EMP1	103	193	13588	4.784747724
NOTCH2, HPN, EMP1	103	37	13588	10.69640514
NOTCH2, HPN, SFN, EMP1	103	108	13588	4.886012226
NOTCH2, HPN, SFN, EMP1	103	161	13588	3.277573419

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
ALDH1A1, RGMA, NOTCH2, PTGS2, UPK1A, PTK7, SFN, KDR	103	271	13588	3.894386128
ALDH1A1, RGMA, NOTCH2, FOXQ1, LY6E, PTK7	103	238	13588	3.325773028
ALDH1A1, RGMA, NOTCH2, MFSD7B, PTK7, PPAP2B, MYC	103	359	13588	2.572301701
ALDH1A1, RGMA, PTK7	103	78	13588	5.073935773
ALDH1A1, RGMA, NOTCH2, PTK7	103	173	13588	3.050227285

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
POLD4, MYD88, CCND2, TNFSF13, BCL6, CD24A, MYC, KDR, CXCL10	103	284	13588	4.180637221
NOTCH2, NUPR1, PTGS2, BCL6, SFN, CD24A, SCGB1A1, H19	103	224	13588	4.711511789
CXCL1, MYD88, NUPR1, C3, CD24A, TRF, CXCL10	103	225	13588	4.10425027
C3, TNFSF13, BCL6, CD24A	103	56	13588	9.423023578
C3, TNFSF13, BCL6, CD24A	103	56	13588	9.423023578
C3, BCL6, CD24A, SCGB1A1	103	57	13588	9.257707375
C3, TNFSF13, BCL6, CD24A	103	65	13588	8.118297237
BCL6, CD24A, SCGB1A1	103	24	13588	16.49029126
CXCL1, NOTCH2, MYD88, NUPR1, C3, CD24A, TRF, CXCL10	103	347	13588	3.041437005
C3, TNFSF13, BCL6, CD24A	103	70	13588	7.538418863
C3, TNFSF13, BCL6	103	30	13588	13.19223301
C3, TNFSF13, BCL6	103	30	13588	13.19223301
MYD88, BCL6, CD24A, SCGB1A1	103	80	13588	6.596116505
MYD88, BCL6, CD24A, SCGB1A1	103	80	13588	6.596116505
MYD88, TNFSF13, BCL6, CD24A, SCGB1A1	103	144	13588	4.580636462
MYD88, BCL6, CD24A, SCGB1A1	103	82	13588	6.435235614
MYD88, C3, TNFSF13, BCL6	103	84	13588	6.282015719
MYD88, C3, TNFSF13, BCL6	103	84	13588	6.282015719

C3, TNFSF13, CD24A	103	34	13588	11.6402056
C3, TNFSF13, CD24A	103	34	13588	11.6402056
C3, TNFSF13, BCL6, CD24A	103	88	13588	5.99646955
MYD88, TNFSF13, BCL6, CD24A, SCGB1A1	103	154	13588	4.283192536
MYD88, TNFSF13, BCL6, CD24A, SCGB1A1	103	156	13588	4.228279811
MYD88, TNFSF13, BCL6, CD24A	103	94	13588	5.613716174
MYD88, TNFSF13, BCL6, CD24A	103	99	13588	5.330195155
BCL6, CD24A, SCGB1A1	103	42	13588	9.423023578
MYD88, TNFSF13, BCL6, CD24A	103	101	13588	5.224646737
C3, BCL6, CD24A, SCGB1A1	103	103	13588	5.123197285
CXCL1, MYD88, NUPR1, C3, PGLYRP1, CD24A, TRF, CXCL10	103	448	13588	2.355755895
MYD88, BCL6, CD24A	103	50	13588	7.915339806
MYD88, BCL6, CD24A	103	50	13588	7.915339806
BCL6, CD24A, SCGB1A1	103	52	13588	7.610903659
MYD88, BCL6, CD24A	103	52	13588	7.610903659
BCL6, CD24A, SCGB1A1	103	53	13588	7.467301704
BCL6, CD24A, SCGB1A1	103	53	13588	7.467301704
TNFSF13, BCL6, CD24A	103	55	13588	7.19576346
MYD88, C3, CD24A	103	57	13588	6.943280531
MYD88, C3, TNFSF13, BCL6, CD24A	103	206	13588	3.201998303
MYD88, C3, TNFSF13	103	63	13588	6.282015719
MYD88, C3, TNFSF13, CD24A	103	136	13588	3.880068532

MYD88, C3, TNFSF13	103	65	13588	6.088722928
MYD88, BCL6, CD24A, SCGB1A1	103	139	13588	3.796326046
MYD88, C3, TNFSF13	103	76	13588	5.207460399
BCL6, CD24A, SCGB1A1	103	76	13588	5.207460399
NUPR1, C3, TRF	103	81	13588	4.886012226
CXCL1, PGLYRP1, TNFSF13, CXCL10	97	180	13288	3.044215349
CXCL1, MYD88, C3, PGLYRP1, TNFSF13, BCL6, CXCL10	103	471	13588	1.96062911
MYD88, C3, TNFSF13	103	89	13588	4.446820116
MYD88, C3, TNFSF13, CD24A	103	186	13588	2.837039357
BCL6, CD24A, SCGB1A1	103	100	13588	3.957669903
BCL6, CD24A, SCGB1A1	103	108	13588	3.664509169
MYD88, C3, TNFSF13	103	126	13588	3.141007859
CXCL1, PLA2G10, C3, PGLYRP1, TNFSF13, HP, SFN, SCGB1A1, TRF, CXCL10, CHAD, MIA1, IGSF1, ACE2, ITIH5, SCGB3A2, CP, WFDC2	108	1680	12504	1.24047619
CXCL1, C3, PGLYRP1, TNFSF13, CP, TRF, CXCL10	108	511	12504	1.585996956
CXCL1, C3, PGLYRP1, TNFSF13, CP, TRF, CHAD, CXCL10	108	774	12504	1.196669538
RGMA, MYD88, TNFSF13, FOSL1, CD24A, MYC	103	633	13588	1.250448627

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
ALDH1A1, RGMA, NOTCH2, PTGS2, UPK1A, PTK7, SFN, KDR	103	271	13588	3.894386128
RGMA, PTK7, KDR	103	171	13588	2.314426844
RGMA, PTK7, KDR	103	264	13588	1.499117387

Bonferroni	Benjamini	FDR
0.00314	0.00314	0.023488
0.004096	0.00205	0.030652
0.110652	0.03833	0.872095
0.495542	0.15724	4.9827
0.990787	0.54214	6.839841
0.587675	0.16238	6.403303
0.878523	0.26003	14.56872

Bonferroni	Benjamini	FDR
0.969462	0.58197	5.136908
1	0.72425	39.72814
1	0.78894	53.97455
1	0.90296	87.06267

Bonferroni	Benjamini	FDR
0.989098	0.59496	6.602516
1	0.73464	41.80964
1	0.79741	58.05468
1	0.90995	85.98536
1	0.92401	91.06533

Bonferroni	Benjamini	FDR
0.752239	0.50224	2.087004
0.789011	0.40468	2.324491
0.999344	0.64903	10.4872
0.999879	0.67608	12.7432
0.999879	0.67608	12.7432
0.999923	0.65084	13.33719
0.999999	0.74251	18.54255
1	0.70504	19.86535
1	0.69206	22.06226
1	0.66883	22.16445
1	0.73401	28.84412
1	0.73401	28.84412
1	0.73142	30.07076
1	0.73142	30.07076
1	0.7262	31.06608
1	0.71712	31.73276
1	0.72229	33.41435
1	0.72229	33.41435

1	0.72696	35.05908
1	0.72696	35.05908
1	0.73311	36.82345
1	0.72065	37.03843
1	0.7209	38.26142
1	0.72396	42.00382
1	0.75818	46.32811
1	0.75709	47.35975
1	0.75279	48.04827
1	0.75902	49.75869
1	0.79589	56.86009
1	0.79463	58.74154
1	0.79463	58.74154
1	0.80908	61.3698
1	0.80908	61.3698
1	0.81184	62.64695
1	0.81184	62.64695
1	0.82487	65.12456
1	0.8369	67.49721
1	0.83502	68.14509
1	0.85565	73.96677
1	0.85466	74.59449

1	0.85935	75.9056
1	0.85769	76.40492
1	0.90824	84.70282
1	0.90824	84.70282
1	0.90119	87.74383
1	0.92493	86.25963
1	0.92379	91.38366
1	0.92233	91.55869
1	0.92966	94.20815
1	0.93758	95.11486
1	0.94593	96.79287
1	0.96478	98.83316
1	0.86472	97.61389
1	0.86255	97.88048
1	0.93779	99.9751
1	0.99345	99.99911

Bonferroni	Benjamini	FDR
0.989098	0.59496	6.602516
1	0.98336	99.93286
1	0.99696	99.99994

Category	Term	Count	%	PValue
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	4	2.030456853	0.001836248
KEGG_PATHWAY	mmu04110:Cell cycle	4	2.030456853	0.00586509
KEGG_PATHWAY	mmu04114:Oocyte meiosis	3	1.52284264	0.044516125
KEGG_PATHWAY	mmu00230:Purine metabolism	3	1.52284264	0.077363358

Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
CDK1, PDE3B, CCNA1, CDC25C	18	85	5738	15.00130719	0.055383282
CDK1, CDC20, CCNA1, CDC25C	18	128	5738	9.961805556	0.166692922
CDK1, CDC20, CDC25C	18	115	5738	8.315942029	0.756261451
NME5, PDE3B, AK7	18	157	5738	6.091295117	0.917595363

Benjamini	FDR
0.055383282	1.566543526
0.087143451	4.927882127
0.375343293	32.37584287
0.464218255	49.9292649

Annotation Cluster 1		Enrichment Score: 7.983752117568295		
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	18	9.1370558	6.13E-11
GOTERM_CC_FAT	GO:0005856~cytoskeleton	25	12.690355	4.38E-10
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	20	10.152284	5.47E-09
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	27	13.705584	9.06E-07
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	27	13.705584	9.06E-07

Annotation Cluster 2		Enrichment Score: 3.8276005110552687		
Category	Term	Count	%	PValue
GOTERM_CC_FAT	GO:0005929~cilium	9	4.5685279	3.99E-07
GOTERM_CC_FAT	GO:0042995~cell projection	13	6.5989848	2.92E-05
GOTERM_CC_FAT	GO:0005930~axoneme	5	2.5380711	3.63E-05
GOTERM_CC_FAT	GO:0044463~cell projection part	7	3.5532995	2.26E-04
GOTERM_CC_FAT	GO:0035085~cilium axoneme	3	1.5228426	0.0060881
GOTERM_CC_FAT	GO:0044441~cilium part	3	1.5228426	0.0186022

Annotation Cluster 3		Enrichment Score: 3.567569413425449		
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0022402~cell cycle process	14	7.106599	7.91E-07

GOTERM_BP_FAT	GO:0007049~cell cycle	17	8.6294416	8.49E-07
GOTERM_BP_FAT	GO:0051301~cell division	10	5.0761421	5.77E-05
GOTERM_BP_FAT	GO:0000279~M phase	10	5.0761421	6.10E-05
GOTERM_BP_FAT	GO:0022403~cell cycle phase	10	5.0761421	1.87E-04
GOTERM_BP_FAT	GO:0000280~nuclear division	7	3.5532995	0.0011372
GOTERM_BP_FAT	GO:0007067~mitosis	7	3.5532995	0.0011372
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	7	3.5532995	0.0012658
GOTERM_BP_FAT	GO:0048285~organelle fission	7	3.5532995	0.0013693
GOTERM_BP_FAT	GO:0051327~M phase of meiotic cell cycle	5	2.5380711	0.0021364
GOTERM_BP_FAT	GO:0007126~meiosis	5	2.5380711	0.0021364
GOTERM_BP_FAT	GO:0051321~meiotic cell cycle	5	2.5380711	0.0023192
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	7	3.5532995	0.0039897

Annotation Cluster 4	Enrichment Score: 3.486575757542855			
Category	Term	Count	%	PValue
GOTERM_MF_FAT	GO:0005524~ATP binding	25	12.690355	6.05E-06
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	25	12.690355	7.40E-06
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	25	12.690355	1.74E-05
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	25	12.690355	2.00E-05
GOTERM_MF_FAT	GO:0001882~nucleoside binding	25	12.690355	2.23E-05

GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	12	6.0913706	6.57E-05
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	26	13.19797	7.88E-05
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	26	13.19797	7.88E-05
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	26	13.19797	1.54E-04
GOTERM_MF_FAT	GO:0000166~nucleotide binding	27	13.705584	6.90E-04
GOTERM_MF_FAT	GO:0004672~protein kinase activity	12	6.0913706	0.0010682
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	11	5.5837563	0.0059688
GOTERM_BP_FAT	GO:0016310~phosphorylation	11	5.5837563	0.0128619
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	12	6.0913706	0.0173029
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	12	6.0913706	0.0173029
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	7	3.5532995	0.044706

Annotation Cluster 5	Enrichment Score: 1.6900010529961471			
Category	Term	Count	%	PValue
GOTERM_MF_FAT	GO:0003774~motor activity	5	2.5380711	0.0113254
GOTERM_CC_FAT	GO:0030286~dynein complex	3	1.5228426	0.0130213
GOTERM_CC_FAT	GO:0005875~microtubule associated complex	3	1.5228426	0.0577152

Annotation Cluster 6	Enrichment Score: 1.4874518500445348			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0007017~microtubule-based process	6	3.0456853	0.0098646
GOTERM_MF_FAT	GO:0003774~motor activity	5	2.5380711	0.0113254

GOTERM_MF_FAT	GO:0003777~microtubule motor activity	3	1.5228426	0.077816
GOTERM_BP_FAT	GO:0007018~microtubule-based movement	3	1.5228426	0.1291193

Annotation Cluster 7	Enrichment Score: 1.2247332442189223			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0007017~microtubule-based process	6	3.0456853	0.0098646
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	5	2.5380711	0.142883
GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	3	1.5228426	0.1502243

Annotation Cluster 8	Enrichment Score: 1.070529108755974			
Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0007368~determination of left/right symmetry	3	1.5228426	0.0289489
GOTERM_BP_FAT	GO:0009799~determination of symmetry	3	1.5228426	0.0302077
GOTERM_BP_FAT	GO:0009855~determination of bilateral symmetry	3	1.5228426	0.0302077
GOTERM_BP_FAT	GO:0007389~pattern specification process	4	2.0304569	0.2566144
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	3	1.5228426	0.6549498

Genes	List Total	Pop Hits	Pop Total
USP2, NEK2, TTLL6, KIF9, SPAG17, TRAF3IP1, SASS6, DNALI1, MAST2, LCA5, TEKT1, CEP170, DNAHC7B, CNTROB, DYNC2H1, TEKT4, CCNA1, MYH10	65	450	12504
USP2, NEK2, FERMT1, NCS1, TTLL6, KIF9, SPAG17, SLC1A4, DNALI1, CEP170, TEKT1, DYNC2H1, MNS1, TEKT4, CCNA1, ELMOD1, UBXN11, RSPH9, TRAF3IP1, SASS6, MAST2, LCA5, CNTROB, DNAHC7B, MYH10	65	1122	12504
NEK2, USP2, NCS1, FERMT1, TTLL6, KIF9, SPAG17, SLC1A4, SASS6, DNALI1, LCA5, TEKT1, CEP170, DNAHC7B, CNTROB, DYNC2H1, MNS1, TEKT4, CCNA1, MYH10	65	774	12504
USP2, NEK2, NCS1, FERMT1, TTLL6, KIF9, SPAG17, SLC1A4, DNALI1, TEKT1, CEP170, DYNC2H1, MNS1, TEKT4, CCNA1, TOP2A, ELMOD1, UBXN11, SMC2, RSPH9, TRAF3IP1, SASS6, MAST2, LCA5, CNTROB, DNAHC7B, MYH10	65	1919	12504
USP2, NEK2, NCS1, FERMT1, TTLL6, KIF9, SPAG17, SLC1A4, DNALI1, TEKT1, CEP170, DYNC2H1, MNS1, TEKT4, CCNA1, TOP2A, ELMOD1, UBXN11, SMC2, RSPH9, TRAF3IP1, SASS6, MAST2, LCA5, CNTROB, DNAHC7B, MYH10	65	1919	12504

Genes	List Total	Pop Hits	Pop Total
EFHC1, ENKUR, LCA5, DNAHC7B, DYNC2H1, TTLL6, TEKT4, SPAG17, RSPH9	65	135	12504
NCS1, FERMT1, TTLL6, SPAG17, RSPH9, EFHC1, ENKUR, LCA5, DNAHC7B, DYNC2H1, TEKT4, KNDC1, MYH10	65	575	12504
EFHC1, LCA5, DYNC2H1, SPAG17, RSPH9	65	37	12504
EFHC1, LCA5, DYNC2H1, TTLL6, SPAG17, RSPH9, MYH10	65	170	12504
LCA5, DYNC2H1, RSPH9	65	23	12504
LCA5, DYNC2H1, RSPH9	65	41	12504

Genes	List Total	Pop Hits	Pop Total
CDK1, MEIG1, NEK2, 4632434I11RIK, CDC20, CDC25C, SMC2, MLF1, RSPH1, CNTROB, MNS1, CCNA1, NEK4, MYH10	85	393	13588

CDK1, MEIG1, NEK2, 4632434I11RIK, CDC20, CDC25C, SMC2, MLF1, SASS6, MCM8, ANKRD54, RSPH1, CNTROB, MNS1, NEK4, CCNA1, MYH10	85	611	13588
CDK1, NEK2, CNTROB, CDC20, NEK4, CCNA1, CDC25C, SMC2, TOP2A, MYH10	85	281	13588
CDK1, MEIG1, NEK2, RSPH1, MNS1, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	283	13588
CDK1, MEIG1, NEK2, RSPH1, MNS1, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	328	13588
CDK1, NEK2, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	190	13588
CDK1, NEK2, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	190	13588
CDK1, NEK2, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	194	13588
CDK1, NEK2, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	197	13588
MEIG1, NEK2, RSPH1, MNS1, CCNA1	85	88	13588
MEIG1, NEK2, RSPH1, MNS1, CCNA1	85	88	13588
MEIG1, NEK2, RSPH1, MNS1, CCNA1	85	90	13588
CDK1, NEK2, CDC20, NEK4, CCNA1, CDC25C, SMC2	85	244	13588

Genes	List Total	Pop Hits	Pop Total
STK33, NEK2, FIGNL1, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1443	13288
STK33, NEK2, FIGNL1, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1460	13288
STK33, NEK2, FIGNL1, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1535	13288
STK33, NEK2, FIGNL1, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1548	13288
STK33, NEK2, FIGNL1, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1558	13288

CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, KNDC1, NEK5, MELK, CDKL4	85	421	13288
STK33, FIGNL1, NEK2, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, RABL5, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1796	13288
STK33, FIGNL1, NEK2, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, RABL5, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1796	13288
STK33, FIGNL1, NEK2, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, RABL5, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, NEK4, NEK5, MELK, MYH10	85	1871	13288
STK33, FIGNL1, NEK2, ULK4, KIF9, TTLL13, CMPK2, MCM8, DYNC2H1, TOP2A, CDK1, MAK, RABL5, NEK10, LRGUK, AK7, SMC2, CDKL4, NME5, IQCA, MAST2, DNAHC7B, RBMX2, NEK4, NEK5, MELK, MYH10	85	2183	13288
CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, KNDC1, NEK5, MELK, CDKL4	85	583	13288
CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, NEK5, MELK, CDKL4	85	640	13588
CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, NEK5, MELK, CDKL4	85	718	13588
CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, CDC25C, NEK5, MELK, CDKL4	85	866	13588
CDK1, STK33, MAST2, MAK, NEK2, NEK10, ULK4, NEK4, CDC25C, NEK5, MELK, CDKL4	85	866	13588
MAST2, FIGNL1, NEK2, FBP1, NEK10, NEK4, NEK5	85	409	13288

Genes	List Total	Pop Hits	Pop Total
DNALI1, DNAHC7B, DYNC2H1, KIF9, MYH10	85	138	13288
DNALI1, DNAHC7B, DYNC2H1	65	34	12504
DNALI1, DNAHC7B, DYNC2H1	65	76	12504

Genes	List Total	Pop Hits	Pop Total
TEKT1, DNAHC7B, CNTROB, DYNC2H1, TEKT4, KIF9	85	211	13588
DNALI1, DNAHC7B, DYNC2H1, KIF9, MYH10	85	138	13288

DNAHC7B, DYNC2H1, KIF9	85	73	13288
DNAHC7B, DYNC2H1, KIF9	85	101	13588

Genes	List Total	Pop Hits	Pop Total
TEKT1, DNAHC7B, CNTROB, DYNC2H1, TEKT4, KIF9	85	211	13588
FOXJ1, TEKT1, CNTROB, TEKT4, MYH10	85	326	13588
TEKT1, CNTROB, TEKT4	85	111	13588

Genes	List Total	Pop Hits	Pop Total
STIL, DYNC2H1, TBX1	85	43	13588
STIL, DYNC2H1, TBX1	85	44	13588
STIL, DYNC2H1, TBX1	85	44	13588
STIL, FOXJ1, DYNC2H1, TBX1	85	284	13588
STIL, DYNC2H1, TBX1	85	359	13588

Fold Enrichment	Bonferroni	Benjamini	FDR
7.694769231	8.15E-09	8.15E-09	7.16E-08
4.286301933	5.83E-08	2.91E-08	5.12E-07
4.970781157	7.27E-07	2.42E-07	6.40E-06
2.706601996	1.21E-04	2.41E-05	0.00106
2.706601996	1.21E-04	2.41E-05	0.00106

Fold Enrichment	Bonferroni	Benjamini	FDR
12.82461538	5.31E-05	1.33E-05	4.67E-04
4.349217391	0.003878	6.47E-04	0.034157
25.995842	0.004818	6.90E-04	0.04245
7.921085973	0.029582	0.00375	0.263647
25.0916388	0.556117	0.07118	6.891497
14.07579737	0.917701	0.16338	19.71281

Fold Enrichment	Bonferroni	Benjamini	FDR
5.69471636	5.24E-04	5.24E-04	0.001184

4.447790507	5.63E-04	2.81E-04	0.001271
5.688926104	0.037544	0.01267	0.086371
5.648721679	0.039615	0.01005	0.091231
4.87374462	0.116641	0.0245	0.279662
5.889535604	0.529706	0.11815	1.689053
5.889535604	0.529706	0.11815	1.689053
5.76810188	0.568179	0.11305	1.878331
5.680262765	0.596859	0.10735	2.030485
9.082887701	0.757785	0.14576	3.151062
9.082887701	0.757785	0.14576	3.151062
8.881045752	0.785496	0.14268	3.416398
4.58611379	0.92938	0.21412	5.809298

Fold Enrichment	Bonferroni	Benjamini	FDR
2.708409767	9.85E-04	9.85E-04	0.007324
2.676873489	0.001206	6.03E-04	0.008965
2.546081625	0.002825	9.42E-04	0.02102
2.524699802	0.003253	8.14E-04	0.024214
2.508495054	0.003622	7.26E-04	0.026964

4.455945228	0.010647	0.00178	0.079515
2.26312066	0.012764	0.00183	0.095422
2.26312066	0.012764	0.00183	0.095422
2.172402301	0.024724	0.00312	0.185874
1.933529142	0.106414	0.01119	0.832638
3.217758047	0.159879	0.01571	1.286279
2.747573529	0.981111	0.28163	8.572736
2.449090611	0.999813	0.45831	17.61804
2.215133813	0.999991	0.53767	22.99568
2.215133813	0.999991	0.53767	22.99568
2.675564505	0.999421	0.35502	42.53594

Fold Enrichment	Bonferroni	Benjamini	FDR
5.664109122	0.843793	0.13308	12.88746
16.97375566	0.825041	0.12549	14.2089
7.593522267	0.999632	0.38992	50.098

Fold Enrichment	Bonferroni	Benjamini	FDR
4.545748536	0.998602	0.39685	13.79275
5.664109122	0.843793	0.13308	12.88746

6.424496374	0.999998	0.50092	62.51746
4.748281887	1	0.98449	87.37815

Fold Enrichment	Bonferroni	Benjamini	FDR
4.545748536	0.998602	0.39685	13.79275
2.451822447	1	0.98587	90.05636
4.320508744	1	0.98163	91.25787

Fold Enrichment	Bonferroni	Benjamini	FDR
11.15294118	1	0.70396	35.58279
10.89946524	1	0.69768	36.82169
10.89946524	1	0.69768	36.82169
2.251532726	1	0.99637	98.81981
1.335867606	1	1	99.99999